



## **RAW SEQUENCE LISTING ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/870,203  
Source: O/PE  
Date Processed by STIC: 6/19/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

SERIAL NUMBER: 09/870,203

**1** \_\_\_\_\_ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
\_\_\_\_\_ **Wrapped Aminos** was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
\_\_\_\_\_ prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 \_\_\_\_\_ Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 \_\_\_\_ Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 \_\_\_\_\_ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 \_\_\_\_\_ Skipped Sequences Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 \_\_\_\_\_ Skipped Sequences Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
(NEW RULES) <210> sequence id number  
<400> sequence id number  
000

9            Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>  
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 9 Use of <220> Sequence(s) 708116 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 \_\_\_\_\_ PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001  
TIME: 12:22:41

Does Not Comply  
Corrected Diskette Needed  
P.6

Input Set : A:\4-31452A.ST25.txt  
Output Set: N:\CRF3\06192001\I870203.raw

3 <110> APPLICANT: Novartis AG  
5 <120> TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins  
7 <130> FILE REFERENCE: 4-31452A  
9 <140> CURRENT APPLICATION NUMBER: US/09/870,203  
9 <141> CURRENT FILING DATE: 2001-05-30  
9 <160> NUMBER OF SEQ ID NOS: 43  
11 <170> SOFTWARE: PatentIn version 3.0  
13 <210> SEQ ID NO: 1  
14 <211> LENGTH: 1746  
15 <212> TYPE: DNA  
16 <213> ORGANISM: Human adenovirus type 5  
18 <220> FEATURE:  
19 <221> NAME/KEY: CDS  
20 <222> LOCATION: (1)..(1746)  
22 <400> SEQUENCE: 1  
23 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48  
24 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro 15 96  
25 1 5 10 15  
27 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 144  
28 Tyr Asp Thr Glu Thr Gly Pro Thr Val Pro Phe Leu Thr Pro Pro 30  
29 20 25 30  
31 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 192  
32 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 45  
33 35 40 45  
35 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 240  
36 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 60  
37 50 55 60  
39 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 288  
40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 75  
41 65 70 75  
43 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 336  
44 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 95  
45 85 90 95  
47 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 384  
48 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 110  
49 100 105 110  
51 act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 432  
52 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 125  
53 115 120 125  
55 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 480  
56 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 140  
57 130 135 140  
59 gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 528  
60 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 160  
61 145 150 155  
63 aca tca ggc ccc ctc acc acc gat agc agt acc ctt act atc act  
64 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001

TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt

Output Set: N:\CRF3\06192001\I870203.raw

65		165		170		175	
67	gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg					576	
68	Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu						
69		180		185		190	
71	aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg					624	
72	Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly						
73		195		200		205	
75	gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act					672	
76	Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr						
77		210		215		220	
79	ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act					720	
80	Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr						
81	225		230		235		240
83	gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca					768	
84	Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala						
85		245		250		255	
87	gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt					816	
88	Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val						
89		260		265		270	
91	agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag					864	
92	Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln						
93		275		280		285	
95	ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac					912	
96	Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn						
97		290		295		300	
99	aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag					960	
100	Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu						
101	305		310		315		320
103	gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata					1008	
104	Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile						
105		325		330		335	
107	gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca					1056	
108	Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro						
109		340		345		350	
111	aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat					1104	
112	Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp						
113		355		360		365	
115	tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac					1152	
116	Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp						
117		370		375		380	
119	agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act					1200	
120	Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr						
121	385		390		395		400
123	ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag					1248	
124	Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu						
125		405		410		415	
127	aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata					1296	
128	Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile						
129		420		425		430	

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001

TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt

Output Set: N:\CRF3\06192001\I870203.raw

```

131 ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata      1344
132 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
133      435      440      445
135 tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat      1392
136 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
137      450      455      460
139 gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt      1440
140 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
141 465      470      475      480
143 aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga      1488
144 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
145      485      490      495
147 ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc      1536
148 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
149      500      505      510
151 aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa      1584
152 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
153      515      520      525
155 cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac      1632
156 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
157      530      535      540
159 aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc      1680
160 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
161 545      550      555      560
163 cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca      1728
164 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
165      565      570      575
167 tac att gcc caa gaa taa      1746
168 Tyr Ile Ala Gln Glu
169      580
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 581
174 <212> TYPE: PRT
175 <213> ORGANISM: Human adenovirus type 5
177 <400> SEQUENCE: 2
179 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
180 1      5      10      15
183 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
184      20      25      30
187 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
188      35      40      45
191 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
192      50      55      60
195 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
196 65      70      75      80
199 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
200      85      90      95
203 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
204      100      105      110

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001

TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt

Output Set: N:\CRF3\06192001\I870203.raw

```

207 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
208      115      120      125
211 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
212      130      135      140
215 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
216 145      150      155      160
219 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
220      165      170      175
223 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
224      180      185      190
227 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
228      195      200      205
231 Ala Pro Leu His Val Thr Asp Leu Asn Thr Leu Thr Val Ala Thr
232      210      215      220
235 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
236 225      230      235      240
239 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
240      245      250      255
243 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
244      260      265      270
247 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
248      275      280      285
251 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
252      290      295      300
255 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
256 305      310      315      320
259 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
260      325      330      335
263 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
264      340      345      350
267 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
268      355      360      365
271 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
272      370      375      380
275 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
276 385      390      395      400
279 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
280      405      410      415
283 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
284      420      425      430
287 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
288      435      440      445
291 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
292      450      455      460
295 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
296 465      470      475      480
299 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
300      485      490      495
303 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001

TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt

Output Set: N:\CRF3\06192001\I870203.raw

```

304          500          505          510
307 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
308          515          520          525
311 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
312          530          535          540
315 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
316 545          550          555          560
319 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
320          565          570          575
323 Tyr Ile Ala Gln Glu
324          580
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 1746
329 <212> TYPE: DNA
C--> 330 <213> ORGANISM: Artificial
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Codes for a mutated Human Adenovirus type 5 fiber protein.
335 <220> FEATURE:
336 <221> NAME/KEY: CDS
337 <222> LOCATION: (1)..(1746)
339 <220> FEATURE:
340 <221> NAME/KEY: mutation
341 <222> LOCATION: (1222)..(1227)
343 <400> SEQUENCE: 3
344 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
345 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
346 1          5          10          15
348 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
349 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
350          20          25          30
352 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct      144
353 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
354          35          40          45
356 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc      192
357 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
358          50          55          60
360 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      240
361 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
362 65          70          75          80
364 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      288
365 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
366          85          90          95
368 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      336
369 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
370          100          105          110
372 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      384
373 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
374          115          120          125
376 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      432

```

09/10/203 6

<210> 4  
<211> 581  
<212> PRT  
<213> Artificial

*see item 11 on Error Summary sheet*

<400> 4

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro



The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001

TIME: 12:22:42

Input Set : A:\4-31452A.ST25.txt

Output Set: N:\CRF3\06192001\I870203.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:330 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
 L:496 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
 L:498 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:498 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:651 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
 L:815 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
 L:817 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:817 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:970 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
 L:1133 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
 L:1135 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:1135 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:1288 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
 L:1452 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
 L:1454 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:1454 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:1607 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
 L:1771 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
 L:1773 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:1773 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:1926 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
 L:2092 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
 L:2094 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2094 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:2247 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
 L:2413 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
 L:2415 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2415 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:2568 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
 L:2732 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
 L:2734 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2734 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:2887 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
 L:3051 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
 L:3053 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:3053 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:3206 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21  
 L:3222 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
 L:3238 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23  
 L:3254 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24  
 L:3270 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
 L:3286 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
 L:3302 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
 L:3318 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28  
 L:3334 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29  
 L:3350 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/870,203

DATE: 06/19/2001

TIME: 12:22:42

Input Set : A:\4-31452A.ST25.txt

Output Set: N:\CRF3\06192001\I870203.raw

L:3366 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31  
L:3382 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32  
L:3398 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33  
L:3414 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34  
L:3430 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35  
L:3446 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36  
L:3462 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37  
L:3478 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38  
L:3494 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39  
L:3510 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40  
L:3526 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41  
L:3542 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42  
L:3558 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43